

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Lee, James  
Wood, William I.

(ii) TITLE OF INVENTION: PF4A Receptors

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Genentech, Inc.  
(B) STREET: 1 DNA Way  
(C) CITY: South San Francisco  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 94080

(v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE: 24-June-1998  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/701265  
(B) FILING DATE: 22-AUG-1996

(vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/664228  
(B) FILING DATE: 06-JUN-1996

(vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/076093  
(B) FILING DATE: 11-JUN-1993

(vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 07/810782  
(B) FILING DATE: 19-DEC-1991

(viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Love, Richard B.  
(B) REGISTRATION NUMBER: 34,659  
(C) REFERENCE/DOCKET NUMBER: P0706P2C2

(ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 415/225-5530  
(B) TELEFAX: 415/952-9881  
(C) TELEX: 910/371-7168

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1933 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

10 CCTGGCCGGT GCTTCAGTTA GATCAAACCA TTGCTGAAAC TGAAGAGGAC 50  
 10 ATGTCAAATA TTACAGATCC ACAGATGTGG GATTTTGATG ATCTAAATTT 100  
 CACTGGCATG CCACCTGCAG ATGAAGATTA CAGCCCCTGT ATGCTAGAAA 150  
 15 CTGAGACACT CAACAAGTAT GTTGTGATCA TCGCCTATGC CCTAGTGTTT 200  
 CTGCTGAGCC TGCTGGGAAA CTCCCTGGTG ATGCTGGTCA TCTTATACAG 250  
 CAGGGTCGGC CGCTCCGTCA CTGATGTCTA CCTGCTGAAC CTGGCCTTGG 300  
 20 CCGACCTACT CTTTGCCCTG ACCTTGCCCA TCTGGGCCGC CTCCAAGGTG 350  
 AATGGCTGGA TTTTGGCAC ATTCTGTGTC AAGGTGGTCT CACTCCTGAA 400  
 25 GGAAGTCAAC TTCTACAGTG GCATCCTGCT GTTGGCCTGC ATCAGTGTGG 450  
 ACCGTTACCT GGCCATTGTC CATGCCACAC GCACACTGAC CCAGAAGCGT 500  
 CACTTGGTCA AGTTTGTGTTG TCTTGGCTGC TGGGGACTGT CTATGAATCT 550  
 30 GTCCCTGCCC TTCTTCCTTT TCCGCCAGGC TTACCATCCA AACAATTCCA 600  
 GTCCAGTTTG CTATGAGGTC CTGGGAAATG ACACAGCAAA ATGGCGGATG 650  
 GTGTTGCGGA TCCTGCCTCA CACCTTTGGC TTCATCGTGC CGCTGTTTGT 700  
 35 CATGCTGTTC TGCTATGGAT TCACCTGCG TACACTGTTT AAGGCCACAC 750  
 TGGGGCAGAA GCACCGAGCC ATGAGGGTCA TCTTTGCTGT CGTCCTCATC 800  
 40 TTCTTGCTTT GCTGGCTGCC CTACAACCTG GTCCTGCTGG CAGACACCCT 850  
 CATGAGGACC CAGGTGATCC AGGAGACCTG TGAGCGCCGC AACCAACATCG 900  
 GCCGGGCCCT GGATGCCACT GAGATTCTGG GATTTCTCCA TAGCTGCCTC 950  
 45 AACCCCATCA TCTACGCCTT CATCGGCCAA AATTTTCGCC ATGGATTCCT 1000  
 CAAGATCCTG GCTATGCATG GCCTGGTCAG CAAGGAGTTC TTGGCACGTC 1050  
 50 ATCGTGTTAC CTCCTACACT TCTTCGTCTG TCAATGTCTC TTCCAACCTC 1100  
 TGAAAACCAT CGATGAAGGA ATATCTCTTC TCAGAAGGAA AGAATAACCA 1150  
 ACACCTGAG GTTGTGTGTG GAAGGTGATC TGGCTCTGGA CAGGCACTAT 1200  
 55 CTGGGTTTTG GGGGGACGCT ATAGGATGTG GGAAGTTAG GAACTGGTGT 1250  
 CTTCAGGGGC CACACCAACC TTCTGAGGAG CTGTTGAGGT ACCTCCAAGG 1300

ACCGGCCTTT GCACCTCCAT GGAAACGAAG CACCATCATT CCCGTTGAAC 1350  
 GTCACATCTT TAACCCACTA ACTGGCTAAT TAGCATGGCC ACATCTGAGC 1400  
 CCCGAATCTG ACATTAGATG AGAGAACAGG GCTGAAGCTG TGTCCTCATG 1450  
 AGGGCTGGAT GCTCTCGTTG ACCCTCACAG GAGCATCTCC TCAACTCTGA 1500  
 GTGTTAAGCG TTGAGCCACC AAGCTGGTGG CTCTGTGTGC TCTGATCCGA 1550  
 GCTCAGGGGG GTGGTTTTCC CATCTCAGGT GTGTTGCAGT GTCTGCTGGA 1600  
 GACATTGAGG CAGGCACTGC CAAAACATCA ACCTGCCAGC TGGCCTTGTG 1650  
 AGGAGCTGGA AACACATGTT CCCCTTGGGG GTGGTGGATG AACAAAGAGA 1700  
 AAGAGGGTTT GGAAGCCAGA TCTATGCCAC AAGAACCCCC TTTACCCCCA 1750  
 TGACCAACAT CGCAGACACA TGTGCTGGCC ACCTGCTGAG CCCCAAGTGG 1800  
 AACGAGACAA GCAGCCCTTA GCCCTTCCCC TCTGCAGCTT CCAGGCTGGC 1850  
 GTGCAGCATC AGCATCCCTA GAAAGCCATG TGCAGCCACC AGTCCATTGG 1900  
 GCAGGCAGAT GTTCCTAATA AAGCTTCTGT TCC 1933

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Asn	Ile	Thr	Asp	Pro	Gln	Met	Trp	Asp	Phe	Asp	Asp	Leu	1	5	10	15
Asn	Phe	Thr	Gly	Met	Pro	Pro	Ala	Asp	Glu	Asp	Tyr	Ser	Pro	Cys	20	25	30	
Met	Leu	Glu	Thr	Glu	Thr	Leu	Asn	Lys	Tyr	Val	Val	Ile	Ile	Ala	35	40	45	
Tyr	Ala	Leu	Val	Phe	Leu	Leu	Ser	Leu	Leu	Gly	Asn	Ser	Leu	Val	50	55	60	
Met	Leu	Val	Ile	Leu	Tyr	Ser	Arg	Val	Gly	Arg	Ser	Val	Thr	Asp	65	70	75	
Val	Tyr	Leu	Leu	Asn	Leu	Ala	Leu	Ala	Asp	Leu	Leu	Phe	Ala	Leu	80	85	90	
Thr	Leu	Pro	Ile	Trp	Ala	Ala	Ser	Lys	Val	Asn	Gly	Trp	Ile	Phe	95	100	105	
Gly	Thr	Phe	Leu	Cys	Lys	Val	Val	Ser	Leu	Leu	Lys	Glu	Val	Asn	110	115	120	

Phe Tyr Ser Gly Ile Leu Leu Leu Ala Cys Ile Ser Val Asp Arg  
 125 130 135  
 Tyr Leu Ala Ile Val His Ala Thr Arg Thr Leu Thr Gln Lys Arg  
 140 145 150  
 5 His Leu Val Lys Phe Val Cys Leu Gly Cys Trp Gly Leu Ser Met  
 155 160 165  
 Asn Leu Ser Leu Pro Phe Phe Leu Phe Arg Gln Ala Tyr His Pro  
 10 170 175 180  
 Asn Asn Ser Ser Pro Val Cys Tyr Glu Val Leu Gly Asn Asp Thr  
 185 190 195  
 15 Ala Lys Trp Arg Met Val Leu Arg Ile Leu Pro His Thr Phe Gly  
 200 205 210  
 Phe Ile Val Pro Leu Phe Val Met Leu Phe Cys Tyr Gly Phe Thr  
 215 220 225  
 20 Leu Arg Thr Leu Phe Lys Ala His Met Gly Gln Lys His Arg Ala  
 230 235 240  
 Met Arg Val Ile Phe Ala Val Val Leu Ile Phe Leu Leu Cys Trp  
 245 250 255  
 25 Leu Pro Tyr Asn Leu Val Leu Leu Ala Asp Thr Leu Met Arg Thr  
 260 265 270  
 Gln Val Ile Gln Glu Thr Cys Glu Arg Arg Asn Asn Ile Gly Arg  
 275 280 285  
 30 Ala Leu Asp Ala Thr Glu Ile Leu Gly Phe Leu His Ser Cys Leu  
 290 295 300  
 35 Asn Pro Ile Ile Tyr Ala Phe Ile Gly Gln Asn Phe Arg His Gly  
 305 310 315  
 Phe Leu Lys Ile Leu Ala Met His Gly Leu Val Ser Lys Glu Phe  
 320 325 330  
 40 Leu Ala Arg His Arg Val Thr Ser Tyr Thr Ser Ser Ser Val Asn  
 335 340 345  
 45 Val Ser Ser Asn Leu  
 350

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1737 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTCCAGT GTGCTGGCGG CGCGGCGCAA AGTGACGCCG AGGGCCTGAG 50  
 TGCTCCAGTA GCCACCGCAT CTGGAGAACC AGCGGTTACC ATGGAGGGGA 100  
 TCAGTATATA CACTTCAGAT AACTACACCG AGGAAATGGG CTCAGGGGAC 150  
 TATGACTCCA TGAAGGAACC CTGTTTCCGT GAAGAAAATG CTAATTTCAA 200  
 TAAAATCTTC CTGCCCACCA TCTACTCCAT CATCTTCTTA ACTGGCATTG 250  
 TGGGCAATGG ATTGGTCATC CTGGTCATGG GTTACCAGAA GAAACTGAGA 300  
 AGCATGACGG ACAAGTACAG GCTGCACCTG TCAGTGGCCG ACCTCCTCTT 350  
 TGTCATCACG CTTCCCTTCT GGGCAGTTGA TGCCGTGGCA AACTGGTACT 400  
 TTGGGAACCTT CCTATGCAAG GCAGTCCATG TCATCTACAC AGTCAACCTC 450  
 TACAGCAGTG TCCTCATCCT GGCCTTCATC AGTCTGGACC GCTACCTGGC 500  
 CATCGTCCAC GCCACCAACA GTCAGAGGCC AAGGAAGCTG TTGGCTGAAA 550  
 AGGTGGTCTA TGTTGGCGTC TGGATCCCTG CCCTCCTGCT GACTATTCCC 600  
 GACTTCATCT TTGCCAACGT CAGTGAGGCA GATGACAGAT ATATCTGTGA 650  
 CCGCTTCTAC CCCAATGACT TGTGGGTGGT TGTGTTCCAG TTTCAGCACA 700  
 TCATGGTTGG CCTTATCCTG CCTGGTATTG TCATCCTGTC CTGCTATTGC 750  
 ATTATCATCT CCAAGCTGTC AACTCCAAG GGCCACCAGA AGCGCAAGGC 800  
 CCTCAAGACC ACAGTCATCC TCATCCTGGC TTTCTTCGCC TGTTGGCTGC 850  
 CTTACTACAT TGGGATCAGC ATCGACTCCT TCATCCTCCT GGAAATCATC 900  
 AAGCAAGGGT GTGAGTTTGA GAACACTGTG CACAAGTGGA TTTCCATCAC 950  
 CGAGGCCCTA GCTTTCTTCC ACTGTTGTCT GAACCCCATC CTCTATGCTT 1000  
 TCCTTGAGC CAAATTTAAA ACCTCTGCCC AGCACGCACT CACCTCTGTG 1050  
 AGCAGAGGGT CCAGCCTCAA GATCCTCTCC AAAGGAAAGC GAGGTGGACA 1100  
 TTCATCTGTT TCCACTGAGT CTGAGTCTTC AAGTTTTTAC TCCAGCTAAC 1150  
 ACAGATGTAA AAGACTTTTT TTTATACGAT AAATAACTTT TTTTAAAGTT 1200  
 ACACATTTTT CAGATATAAA AGACTGACCA ATATTGTACA GTTTTTATTG 1250  
 CTTGTTGGAT TTTTGTCTTG TGTTTCTTTA GTTTTTGTGA AGTTTAATTG 1300  
 ACTTATTTAT ATAAATTTTT TTTGTTTCAT ATTGATGTGT GTCTAGGCAG 1350  
 GACCTGTGGC CAAGTTCTTA GTTGCTGTAT GTCTCGTGGT AGGACTGTAG 1400  
 AAAAGGGAAC TGAACATTCC AGAGCGTGTA GTGAATCACG TAAAGCTAGA 1450  
 AATGATCCCC AGCTGTTTAT GCATAGATAA TCTCTCCATT CCCGTGGAAC 1500

GTTTTTCCTG TTCTTAAGAC GTGATTTTGC TGTAAGAGAT GGCACTTATA 1550  
 ACCAAAGCCC AAAGTGGTAT AGAAATGCTG GTTTTTCAGT TTTCAGGAGT 1600  
 GGGTTGATTT CAGCACCTAC AGTGACAGT CTTGTATTAA GTTGTTAATA 1650  
 AAAGTACATG TTAAACTTAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1700  
 AAAAAAAAAA AAAGCGGCCG CCAGCACACT GGAATTC 1737

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 352 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Glu	Gly	Ile	Ser	Ile	Tyr	Thr	Ser	Asp	Asn	Tyr	Thr	Glu	Glu	1	5	10	15
Met	Gly	Ser	Gly	Asp	Tyr	Asp	Ser	Met	Lys	Glu	Pro	Cys	Phe	Arg	20	25	30	
Glu	Glu	Asn	Ala	Asn	Phe	Asn	Lys	Ile	Phe	Leu	Pro	Thr	Ile	Tyr	35	40	45	
Ser	Ile	Ile	Phe	Leu	Thr	Gly	Ile	Val	Gly	Asn	Gly	Leu	Val	Ile	50	55	60	
Leu	Val	Met	Gly	Tyr	Gln	Lys	Lys	Leu	Arg	Ser	Met	Thr	Asp	Lys	65	70	75	
Tyr	Arg	Leu	His	Leu	Ser	Val	Ala	Asp	Leu	Leu	Phe	Val	Ile	Thr	80	85	90	
Leu	Pro	Phe	Trp	Ala	Val	Asp	Ala	Val	Ala	Asn	Trp	Tyr	Phe	Gly	95	100	105	
Asn	Phe	Leu	Cys	Lys	Ala	Val	His	Val	Ile	Tyr	Thr	Val	Asn	Leu	110	115	120	
Tyr	Ser	Ser	Val	Leu	Ile	Leu	Ala	Phe	Ile	Ser	Leu	Asp	Arg	Tyr	125	130	135	
Leu	Ala	Ile	Val	His	Ala	Thr	Asn	Ser	Gln	Arg	Pro	Arg	Lys	Leu	140	145	150	
Leu	Ala	Glu	Lys	Val	Val	Tyr	Val	Gly	Val	Trp	Ile	Pro	Ala	Leu	155	160	165	
Leu	Leu	Thr	Ile	Pro	Asp	Phe	Ile	Phe	Ala	Asn	Val	Ser	Glu	Ala	170	175	180	
Asp	Asp	Arg	Tyr	Ile	Cys	Asp	Arg	Phe	Tyr	Pro	Asn	Asp	Leu	Trp	185	190	195	
Val	Val	Val	Phe	Gln	Phe	Gln	His	Ile	Met	Val	Gly	Leu	Ile	Leu				

	200	205	210
	Pro Gly Ile Val	Ile Leu Ser Cys Tyr	Cys Ile Ile Ile Ser Lys
	215	220	225
5	Leu Ser His Ser	Lys Gly His Gln Lys	Arg Lys Ala Leu Lys Thr
	230	235	240
	Thr Val Ile Leu	Ile Leu Ala Phe Phe	Ala Cys Trp Leu Pro Tyr
	245	250	255
10	Tyr Ile Gly Ile	Ser Ile Asp Ser Phe	Ile Leu Leu Glu Ile Ile
	260	265	270
	Lys Gln Gly Cys	Glu Phe Glu Asn Thr	Val His Lys Trp Ile Ser
15	275	280	285
	Ile Thr Glu Ala	Leu Ala Phe Phe His	Cys Cys Leu Asn Pro Ile
	290	295	300
20	Leu Tyr Ala Phe	Leu Gly Ala Lys Phe	Lys Thr Ser Ala Gln His
	305	310	315
	Ala Leu Thr Ser	Val Ser Arg Gly Ser	Ser Leu Lys Ile Leu Ser
	320	325	330
25	Lys Gly Lys Arg	Gly Gly His Ser Ser	Val Ser Thr Glu Ser Glu
	335	340	345
	Ser Ser Ser Phe	His Ser Ser	
30	350	352	

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1679 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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GAATTCCAGT GTGCTGGCGG CCGCCCAGTG TGCTGGCGGC GGCAGTTGAG 50
GGAAAGGACA GAGGTTATGA GTGCCTGCAA GAGTGGCAGC CTGGAGTAGA 100
GAAAACACTA AAGGTGGAGT CAAAAGACCT GAGTTCAAGT CCCAGCTCTG 150
CCACTGGTTA GCTGTGGGAT CTCGGAAAAG ACCCAGTGAA AAAAAAAAAA 200
AAAGTGATGA GTTGTGAGGC AGGTCGCGGC CCTACTGCCT CAGGAGACGA 250
TGCGCAGCTC ATTTGCTTAA ATTTGCAGCT GACGGCTGCC ACCTCTCTAG 300
AGGCACCTGG CGGGGAGCCT CTCAACATAA GACAGTGACC AGTCTGGTGA 350
CTCACAGCCG GCACAGCCAT GAACTACCCG CTAACGCTGG AAATGGACCT 400

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5  
 10  
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CGAGAACCTG GAGGACCTGT TCTGGGAACT GGACAGATTG GACAACTATA 450  
 ACGACACCTC CCTGGTGGAA AATCATCTCT GCCCTGCCAC AGAGGGGCCC 500  
 CTCATGGCCT CCTTCAAGGC CGTGTTCTGT CCCGTGGCCT ACAGCCTCAT 550  
 CTTCTCTCTG GGCCTGATCG GCAACGTCCT GGTGCTGGTG ATCCTGGAGC 600  
 GGCACCGGCA GACACGCAGT TCCACGGAGA CTTCTCTGTT CCACCTGGCC 650  
 GTGGCCGACC TCCTGCTGGT CTTTCATCTTG CCCTTTGCCG TGGCCGAGGG 700  
 CTCTGTGGGC TGGGTCTCTG GGACCTTCCT CTGCAAACT GTGATTGCCC 750  
 TGCACAAAGT CAACTTCTAC TGCAGCAGCC TGCTCCTGGC CTGCATCGCC 800  
 GTGGACCGCT ACCTGGCCAT TGTCCACGCC GTCCATGCCT ACCGCCACCG 850  
 CCGCTCTCTC TCCATCCACA TCACCTGTGG GACCATCTGG CTGGTGGGCT 900  
 TCCTCTTTGC CTTGCCAGAG ATTCTCTTCG CCAAAGTCAG CCAAGGCCAT 950  
 CACAACAACT CCCTGCCACG TTGCACCTTC TCCAAGAGA ACCAAGCAGA 1000  
 AACGCATGCC TGGTTCACCT CCCGATTCTT CTACCATGTG GCGGGATTCC 1050  
 TGCTGCCCAT GCTGGTGATG GGCTGGTGCT ACGTGGGGGT AGTGACAGG 1100  
 TTGCGCCAGG CCCAGCGGCG CCCTCAGCGG CAGAAGGCAG TCAGGGTGGC 1150  
 CATCTGGTG ACAAGCATCT TCTTCTCTG CTGGTCACCC TACCACATCG 1200  
 TCATCTTCCT GGACACCCTG GCGAGGCTGA AGGCCGTGGA CAATACCTGC 1250  
 AAGCTGAATG GCTCTCTCCC CGTGGCCATC ACCATGTGTG AGTTCCTGGG 1300  
 CCTGGCCCAC TGCTGCCTCA ACCCCATGCT CTACACTTTC GCCGGCGTGA 1350  
 AGTTCCGCAG TGACCTGTCG CGGCTCCTGA CGAAGCTGGG CTGTACCGGC 1400  
 CCTGCCTCCC TGTGCCAGCT CTTCCCTAGC TGGCGCAGGA GCAGTCTCTC 1450  
 TGAGTCAGAG AATGCCACCT CTCTCACCAC GTTCTAGGTC CCAGTGTCCT 1500  
 CTTTTATTGC TGCTTTTCCT TGGGGCAGGC AGTGATGCTG GATGCTCCTT 1550  
 CCAACAGGAG CTGGGATCCT AAGGGCTCAC CGTGGCTAAG AGTGTCTTAG 1600  
 GAGTATCCTC ATTTGGGGTA GCTAGAGGAA CCAACCCCCA TTTCTAGAAC 1650  
 ATCCCGCGGC CGCCAGCACA CTGGAATTC 1679

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 372 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

	Met	Asn	Tyr	Pro	Leu	Thr	Leu	Glu	Met	Asp	Leu	Glu	Asn	Leu	Glu	
	1				5					10					15	
5	Asp	Leu	Phe	Trp	Glu	Leu	Asp	Arg	Leu	Asp	Asn	Tyr	Asn	Asp	Thr	
					20					25					30	
	Ser	Leu	Val	Glu	Asn	His	Leu	Cys	Pro	Ala	Thr	Glu	Gly	Pro	Leu	
					35					40					45	
10	Met	Ala	Ser	Phe	Lys	Ala	Val	Phe	Val	Pro	Val	Ala	Tyr	Ser	Leu	
					50					55					60	
	Ile	Phe	Leu	Leu	Gly	Val	Ile	Gly	Asn	Val	Leu	Val	Leu	Val	Ile	
15					65					70					75	
	Leu	Glu	Arg	His	Arg	Gln	Thr	Arg	Ser	Ser	Thr	Glu	Thr	Phe	Leu	
					80					85					90	
20	Phe	His	Leu	Ala	Val	Ala	Asp	Leu	Leu	Leu	Val	Phe	Ile	Leu	Pro	
					95					100					105	
	Phe	Ala	Val	Ala	Glu	Gly	Ser	Val	Gly	Trp	Val	Leu	Gly	Thr	Phe	
					110					115					120	
25	Leu	Cys	Lys	Thr	Val	Ile	Ala	Leu	His	Lys	Val	Asn	Phe	Tyr	Cys	
					125					130					135	
	Ser	Ser	Leu	Leu	Leu	Ala	Cys	Ile	Ala	Val	Asp	Arg	Tyr	Leu	Ala	
30					140					145					150	
	Ile	Val	His	Ala	Val	His	Ala	Tyr	Arg	His	Arg	Arg	Leu	Leu	Ser	
					155					160					165	
35	Ile	His	Ile	Thr	Cys	Gly	Thr	Ile	Trp	Leu	Val	Gly	Phe	Leu	Leu	
					170					175					180	
	Ala	Leu	Pro	Glu	Ile	Leu	Phe	Ala	Lys	Val	Ser	Gln	Gly	His	His	
					185					190					195	
40	Asn	Asn	Ser	Leu	Pro	Arg	Cys	Thr	Phe	Ser	Gln	Glu	Asn	Gln	Ala	
					200					205					210	
	Glu	Thr	His	Ala	Trp	Phe	Thr	Ser	Arg	Phe	Leu	Tyr	His	Val	Ala	
45					215					220					225	
	Gly	Phe	Leu	Leu	Pro	Met	Leu	Val	Met	Gly	Trp	Cys	Tyr	Val	Gly	
					230					235					240	
50	Val	Val	His	Arg	Leu	Arg	Gln	Ala	Gln	Arg	Arg	Pro	Gln	Arg	Gln	
					245					250					255	
	Lys	Ala	Val	Arg	Val	Ala	Ile	Leu	Val	Thr	Ser	Ile	Phe	Phe	Leu	
					260					265					270	
55	Cys	Trp	Ser	Pro	Tyr	His	Ile	Val	Ile	Phe	Leu	Asp	Thr	Leu	Ala	
					275					280					285	

